

SEQUENCE LISTING



<110> Glaxo Group Ltd
 Tate, Simon N
 Delany, Natalie S
 Sanseau, P

<120> Novel Receptors

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<151> 1998-12-01

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 His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
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Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu
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 Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu
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 Asp Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu
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 Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu
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 Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu
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 Leu Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn
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 Ala Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile
 195 200 205

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 Gly Ala Asp Val Gln Ala Ala Ala His Gly Asp Phe Phe Lys Lys Thr
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 Ala Cys Thr Asn Gln Leu Gly Ile Val Lys Phe Leu Leu Gln Asn Ser
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 Trp Gln Thr Ala Asp Ile Ser Ala Arg Asp Ser Val Gly Asn Thr Val
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 His Pro Thr Leu Lys Leu Glu Glu Leu Thr Asn Lys Lys Gly Met Thr
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 Pro Leu Ala Leu Ala Ala Gly Thr Gly Lys Ile Gly Val Leu Ala Tyr
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 Ile Leu Gln Arg Glu Ile Gln Glu Pro Glu Cys Arg His Leu Ser Arg
 355 360 365
 Lys Phe Thr Glu Trp Ala Tyr Gly Pro Val His Ser Ser Leu Tyr Asp
 370 375 380
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 Arg Ile Phe Tyr Phe Asn Phe Leu Val Tyr Cys Leu Tyr Met Ile Ile
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490

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Leu Gln Arg Arg Pro Ser Met Lys Thr Leu Phe Val Asp Ser Tyr Ser

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Glu Met Leu Phe Phe Leu Gln Ser Leu Phe Met Leu Ala Thr Val Val

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Leu Tyr Phe Ser His Leu Lys Glu Tyr Val Ala Ser Met Val Phe Ser

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Leu Ala Leu Gly Trp Thr Asn Met Leu Tyr Tyr Thr Arg Gly Phe Gln

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550

555

560

Gln Met Gly Ile Tyr Ala Val Met Ile Glu Lys Met Ile Leu Arg Asp

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570

575

Leu Cys Arg Phe Met Phe Val Tyr Ile Val Phe Leu Phe Gly Phe Ser

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585

590

Thr Ala Val Val Thr Leu Ile Glu Asp Gly Lys Asn Asp Ser Leu Pro

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600

605

Ser Glu Ser Thr Ser His Arg Trp Arg Gly Pro Ala Cys Arg Pro Pro

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615

620

Asp Ser Ser Tyr Asn Ser Leu Tyr Ser Thr Cys Leu Glu Leu Phe Lys

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630

635

640

Phe Thr Ile Gly Met Gly Asp Leu Glu Phe Thr Glu Asn Tyr Asp Phe

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650

655

Lys Ala Val Phe Ile Ile Leu Leu Leu Ala Tyr Val Ile Leu Thr Tyr

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665

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Ile Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu Thr Val Asn

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680

685

B1

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Asp Asp Tyr Arg Trp Cys Phe Arg Val Asp Glu Val Asn Trp Thr Thr
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Trp Asn Thr Asn Val Gly Ile Ile Asn Glu Asp Pro Gly Asn Cys Glu
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Gly Val Lys Arg Thr Leu Ser Phe Ser Leu Arg Ser Ser Arg Val Ser
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Gly Arg His Trp Lys Asn Phe Ala Leu Val Pro Leu Leu Arg Glu Ala
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Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Ser Pro Leu Asp Cys Pro
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Tyr Glu Glu Gly Gly Leu Ala Ser Cys Pro Ile Ile Thr Val Ser Ser
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Val Leu Thr Ile Gln Arg Pro Gly Asp Gly Pro Ala Ser Val Arg Pro
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Ser Ser Gln Asp Ser Val Ser Ala Gly Glu Lys Pro Pro Arg Leu Tyr
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Asp Arg Arg Ser Ile Phe Asp Ala Val Ala Gln Ser Asn Cys Gln Glu
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Leu Glu Ser Leu Leu Pro Phe Leu Gln Arg Ser Lys Lys Arg Leu Thr
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Asp Ser Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu Lys
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Ala Met Leu Asn Leu His Asn Gly Gln Asn Asp Thr Ile Ala Leu Leu
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Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile Ala

B1

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Pro Leu Asn Arg Leu Leu Gln Asp Lys Trp Asp Arg Phe Val Lys Arg
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Ile Phe Tyr Phe Asn Phe Phe Val Tyr Cys Leu Tyr Met Ile Ile Phe
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465 470 475 480

Ser Val Ser Gly Gly Val Tyr Phe Phe Phe Arg Gly Ile Gln Tyr Phe
485 490 495

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Leu Cys Arg Phe Met Phe Val Tyr Leu Val Phe Leu Phe Gly Phe Ser
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Thr Ala Val Val Thr Leu Ile Glu Asp Gly Lys Asn Asn Ser Leu Pro
595 600 605

B1

Met Glu Ser Thr Pro His Lys Cys Arg Gly Ser Ala Cys Lys Pro Gly
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Asn Ser Tyr Asn Ser Leu Tyr Ser Thr Cys Leu Glu Leu Phe Lys Phe
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gagtgtgtgc aggccaggga gggctttcca gaggagccca gttgagctgg aacaccagtg 180

gggaggagtt gaccagcaaa ggtgcaggga gggatcagca ctttgactg gggagcagag 240

tttgtgcact ggggaagtca actcaagtat tggagcctca gtttcctggt ctgtaaaatg 300

ggttcatcat gacagtgttt gatgaggaaa aggactgccg gcctacacag caagtccaca 360

tggattttct gagcccctcc tgtgcctgaa gcccacgggt aatggttctg ccttagcagg 420

tgcttaccac gtgccaggca ctgcactgca ctggccactg gactgcatgt tctgtccatg 480

aggcttggat atccccatct tacagatcag gaagctgagg ctatgaaatg tcgacttgct 540

B1

caatgtcatg gaatgactaa gtgtggagcc tggatttgaa cttggctctc tggggctcca 600

aagctggctt tcttggtcag cagtaggggc tgggatccaa gtatgggggc ccagcttgac 660

cctgaagtcc accctctttc agcta atg ccc agg gta gtt gga cct ggg gcc 712

Met Pro Arg Val Val Gly Pro Gly Ala

1

5

B1

aat ttg tgt ttc ,cag gtt cgt gaa aga ggc tcc tgt tgc agt tcc cgc 760
 Asn Leu Cys Phe Gln Val Arg Glu Arg Gly Ser Cys Cys Ser Ser Arg
 10 15 20 25

ctg agg ctg gcg gcc aac cac atc tgg gag tgg cct ccc tgt gcc cct 808
 Leu Arg Leu Ala Ala Asn His Ile Trp Glu Trp Pro Pro Cys Ala Pro
 30 35 40

gtc att aca acg gtg gct ttg aag cag ctg gca gca ctg ctg ctt gtc 856
 Val Ile Thr Thr Val Ala Leu Lys Gln Leu Ala Ala Leu Leu Leu Val
 45 50 55

cac gtg gga ggg ggc ttc ctg gag ccc ccg ccc ctg gcc ggg ttc tgc 904
 His Val Gly Gly Gly Phe Leu Glu Pro Pro Pro Leu Ala Gly Phe Cys
 60 65 70

ctg act ccc ctt tca ttc cct tgc agg ctg agc agt gca gac ggg cct 952
 Leu Thr Pro Leu Ser Phe Pro Cys Arg Leu Ser Ser Ala Asp Gly Pro
 75 80 85

ggg gca ggc atg gcg gat tcc agc gaa ggc ccc cgc gcg ggg ccc ggg 1000
 Gly Ala Gly Met Ala Asp Ser Ser Glu Gly Pro Arg Ala Gly Pro Gly
 90 95 100 105

gag gtg gct gag ctc ccc ggg gat gag agt ggc acc cca ggt ggg gag 1048
 Glu Val Ala Glu Leu Pro Gly Asp Glu Ser Gly Thr Pro Gly Gly Glu
 110 115 120

gct ttt cct ctc tcc tcc ctg gcc aat ctg ttt gag ggg gag gat ggc 1096
 Ala Phe Pro Leu Ser Ser Leu Ala Asn Leu Phe Glu Gly Glu Asp Gly
 125 130 135

tcc ctt tcg ccc tca ccg gct gat gcc agt cgc cct gct ggc cca ggc 1144
 Ser Leu Ser Pro Ser Pro Ala Asp Ala Ser Arg Pro Ala Gly Pro Gly
 140 145 150

B1

gat ggg cga cca aat ctg cgc atg aag ttc cag ggc gcc ttc cgc aag 1192
 Asp Gly Arg Pro Asn Leu Arg Met Lys Phe Gln Gly Ala Phe Arg Lys
 155 160 165

ggg gtg ccc aac ccc atc gat ctg ctg gag tcc acc cta tat gag tcc 1240
 Gly Val Pro Asn Pro Ile Asp Leu Leu Glu Ser Thr Leu Tyr Glu Ser
 170 175 180 185

tcg gtg gtg cct ggg ccc aag aaa gca ccc atg gac tca ctg ttt gac 1288
 Ser Val Val Pro Gly Pro Lys Lys Ala Pro Met Asp Ser Leu Phe Asp
 190 195 200

tac ggc acc tat cgt cac cac tcc agt gac aac aag agg tgg agg aag 1336
 Tyr Gly Thr Tyr Arg His His Ser Ser Asp Asn Lys Arg Trp Arg Lys
 205 210 215

B1 aag atc ata gag aag cag ccg cag agc ccc aaa gcc cct gcc cct cag 1384
 Lys Ile Ile Glu Lys Gln Pro Gln Ser Pro Lys Ala Pro Ala Pro Gln
 220 225 230

ccg ccc ccc atc ctc aaa gtc ttc aac cgg cct atc ctc ttt gac atc 1432
 Pro Pro Pro Ile Leu Lys Val Phe Asn Arg Pro Ile Leu Phe Asp Ile
 235 240 245

gtg tcc cgg ggc tcc act gct gac ctg gac ggg ctg ctc cca ttc ttg 1480
 Val Ser Arg Gly Ser Thr Ala Asp Leu Asp Gly Leu Leu Pro Phe Leu
 250 255 260 265

ctg acc cac aag aaa cgc cta act gat gag gag ttt cga gag cca tct 1528
 Leu Thr His Lys Lys Arg Leu Thr Asp Glu Glu Phe Arg Glu Pro Ser
 270 275 280

acg ggg aag acc tgc ctg ccc aag gcc ttg ctg aac ctg agc aat ggc 1576
 Thr Gly Lys Thr Cys Leu Pro Lys Ala Leu Leu Asn Leu Ser Asn Gly
 285 290 295

cgc aac gac acc atc cct gtg ctg ctg gac atc gcg gag cgc acc ggc 1624
 Arg Asn Asp Thr Ile Pro Val Leu Leu Asp Ile Ala Glu Arg Thr Gly
 300 305 310

aac atg cgg gag ttc att aac tcg ccc ttc cgt gac atc tac tat cga 1672
 Asn Met Arg Glu Phe Ile Asn Ser Pro Phe Arg Asp Ile Tyr Tyr Arg
 315 320 325

ggt cag aca gcc ctg cac atc gcc att gag cgt cgc tgc aaa cac tac 1720
 Gly Gln Thr Ala Leu His Ile Ala Ile Glu Arg Arg Cys Lys His Tyr
 330 335 340 345

gtg gaa ctt ctc gtg gcc cag gga gct gat gtc cac gcc cag gcc cgt 1768
 Val Glu Leu Leu Val Ala Gln Gly Ala Asp Val His Ala Gln Ala Arg
 350 355 360

131 ggg cgc ttc ttc cag ccc aag gat gag ggg ggc tac ttc tac ttt ggg 1816
 Gly Arg Phe Phe Gln Pro Lys Asp Glu Gly Gly Tyr Phe Tyr Phe Gly
 365 370 375

gag ctg ccc ctg tcg ctg gct gcc tgc acc aac cag ccc cac att gtc 1864
 Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Asn Gln Pro His Ile Val
 380 385 390

aac tac ctg acg gag aac ccc cac aag aag gcg gac atg cgg cgc cag 1912
 Asn Tyr Leu Thr Glu Asn Pro His Lys Lys Ala Asp Met Arg Arg Gln
 395 400 405

gac tcg cga ggc aac aca gtg ctg cat gcg ctg gtg gcc att gct gac 1960
 Asp Ser Arg Gly Asn Thr Val Leu His Ala Leu Val Ala Ile Ala Asp
 410 415 420 425

aac acc cgt gag aac acc aag ttt gtt acc aag atg tac gac ctg ctg 2008
 Asn Thr Arg Glu Asn Thr Lys Phe Val Thr Lys Met Tyr Asp Leu Leu
 430 435 440

ctg ctc aag tgt gcc cgc ctc ttc ccc gac agc aac ctg gag gcc gtg 2056
 Leu Leu Lys Cys Ala Arg Leu Phe Pro Asp Ser Asn Leu Glu Ala Val
 445 450 455

ctc aac aac gac ggc ctc tcg ccc ctc atg atg gct gcc aag acg ggc 2104
 Leu Asn Asn Asp Gly Leu Ser Pro Leu Met Met Ala Ala Lys Thr Gly
 460 465 470

aag att ggg atc ttt cag cac atc atc cgg cgg gag gtg acg gat gag 2152
 Lys Ile Gly Ile Phe Gln His Ile Ile Arg Arg Glu Val Thr Asp Glu
 475 480 485

gac aca cgg cac ctg tcc cgc aag tcc aag gac tgg gcc tat ggg cca 2200
 Asp Thr Arg His Leu Ser Arg Lys Ser Lys Asp Trp Ala Tyr Gly Pro
 490 495 500 505

gtg tat tcc tcg ctt tat gac ctc tcc tcc ctg gac acg tgt ggg gaa 2248
 Val Tyr Ser Ser Leu Tyr Asp Leu Ser Ser Leu Asp Thr Cys Gly Glu
 510 515 520

gag gcc tcc gtg ctg gag atc ctg gtg tac aac agc aag att gag aac 2296
 Glu Ala Ser Val Leu Glu Ile Leu Val Tyr Asn Ser Lys Ile Glu Asn
 525 530 535

cgc cac gag atg ctg gct gtg gag ccc atc aat gaa ctg ctg cgg gac 2344
 Arg His Glu Met Leu Ala Val Glu Pro Ile Asn Glu Leu Leu Arg Asp
 540 545 550

aag tgg cgg aag ttc ggg gcc gtc tcc ttc tac atc aac gtg gtc tcc 2392
 Lys Trp Arg Lys Phe Gly Ala Val Ser Phe Tyr Ile Asn Val Val Ser
 555 560 565

tac ctg tgt gcc atg gtt atc ttc act ctc acc gcc tac tac cag ccg 2440
 Tyr Leu Cys Ala Met Val Ile Phe Thr Leu Thr Ala Tyr Tyr Gln Pro
 570 575 580 585

B1

ctg gag ggc aca ccg ccg tac cct tac cgc acc acg gtg gac tac ctg 2488
 Leu Glu Gly Thr Pro Pro Tyr Pro Tyr Arg Thr Thr Val Asp Tyr Leu
 590 595 600

cgg ctg gct ggc gag gtc att acg ctc ttc act ggg gtc ctg ttc ttc 2536
 Arg Leu Ala Gly Glu Val Ile Thr Leu Phe Thr Gly Val Leu Phe Phe
 605 610 615

ttc acc aac atc aaa gac ttg ttc atg aag aaa tgc cct gga gtg aat 2584
 Phe Thr Asn Ile Lys Asp Leu Phe Met Lys Lys Cys Pro Gly Val Asn
 620 625 630

tct ctc ttc att gat ggc tcc ttc cag ctg ctc tac ttc atc tac tct 2632
 Ser Leu Phe Ile Asp Gly Ser Phe Gln Leu Leu Tyr Phe Ile Tyr Ser
 635 640 645

gtc ctg gtg atc gtc tca gca gcc ctc tac ctg gca ggg atc gag gcc 2680
 Val Leu Val Ile Val Ser Ala Ala Leu Tyr Leu Ala Gly Ile Glu Ala
 650 655 660 665

tac ctg gcc atg atg gtc ttt gcc ctg gtc ctg ggc tgg atg aat gcc 2728
 Tyr Leu Ala Met Met Val Phe Ala Leu Val Leu Gly Trp Met Asn Ala
 670 675 680

ctt tac ttc acc cgt ggg ctg aag ctg acg ggg acc tat agc atc atg 2776
 Leu Tyr Phe Thr Arg Gly Leu Lys Leu Thr Gly Thr Tyr Ser Ile Met
 685 690 695

atc cag aag att ctc ttc aag gac ctt ttc cga ttc ctg ctc gtc tac 2824
 Ile Gln Lys Ile Leu Phe Lys Asp Leu Phe Arg Phe Leu Leu Val Tyr
 700 705 710

ttg ctc ttc atg atc ggc tac gct tca gcc ctg gtc tcc ctc ctg aac 2872
 Leu Leu Phe Met Ile Gly Tyr Ala Ser Ala Leu Val Ser Leu Leu Asn
 715 720 725

B1

ccg tgt gcc aac atg aag gtg tgc aat gag gac cag acc aac tgc aca 2920
 Pro Cys Ala Asn Met Lys Val Cys Asn Glu Asp Gln Thr Asn Cys Thr
 730 735 740 745

gtg ccc act tac ccc tcg tgc cgt gac agc gag acc ttc agc acc ttc 2968
 Val Pro Thr Tyr Pro Ser Cys Arg Asp Ser Glu Thr Phe Ser Thr Phe
 750 755 760

ctc ctg gac ctg ttt aag ctg acc atc ggc atg ggc gac ctg gag atg 3016
 Leu Leu Asp Leu Phe Lys Leu Thr Ile Gly Met Gly Asp Leu Glu Met
 765 770 775

ctg agc agc acc aag tac ccc gtg gtc ttc atc atc ctg ctg gtg acc 3064
 Leu Ser Ser Thr Lys Tyr Pro Val Val Phe Ile Ile Leu Leu Val Thr
 780 785 790

B1 tac atc atc ctc acc tct gtg ctg ctc ctc aac atg ctc att gcc ctc 3112
 Tyr Ile Ile Leu Thr Ser Val Leu Leu Leu Asn Met Leu Ile Ala Leu
 795 800 805

atg ggc gag aca gtg ggc cag gtc tcc aag gag agc aag cac atc tgg 3160
 Met Gly Glu Thr Val Gly Gln Val Ser Lys Glu Ser Lys His Ile Trp
 810 815 820 825

aag ctg cag tgg gcc acc acc atc ctg gac att gag cgc tcc ttc ccc 3208
 Lys Leu Gln Trp Ala Thr Thr Ile Leu Asp Ile Glu Arg Ser Phe Pro
 830 835 840

gta ttc ctg agg aag gcc ttc cgc tct ggg gag atg gtc acc gtg ggc 3256
 Val Phe Leu Arg Lys Ala Phe Arg Ser Gly Glu Met Val Thr Val Gly
 845 850 855

aag agc tcg gac ggc act cct gac cgc agg tgg tgc ttc agg gtg gat 3304
 Lys Ser Ser Asp Gly Thr Pro Asp Arg Arg Trp Cys Phe Arg Val Asp
 860 865 870

gag gtg aac tgg tct cac tgg aac cag aac ttg ggc atc atc aac gag 3352
 Glu Val Asn Trp Ser His Trp Asn Gln Asn Leu Gly Ile Ile Asn Glu
 875 880 885

gac ccg ggc aag aat gag acc tac cag tat tat ggc ttc tcg cat acc 3400
 Asp Pro Gly Lys Asn Glu Thr Tyr Gln Tyr Tyr Gly Phe Ser His Thr
 890 895 900 905

gtg ggc cgc ctc cgc agg gat cgc tgg tcc tcg gtg gta ccc cgc gtg 3448
 Val Gly Arg Leu Arg Arg Asp Arg Trp Ser Ser Val Val Pro Arg Val
 910 915 920

gtg gaa ctg aac aag aac tcg aac ccg gac gag gtg gtg gtg cct ctg 3496
 Val Glu Leu Asn Lys Asn Ser Asn Pro Asp Glu Val Val Val Pro Leu
 925 930 935

B1 gag agc atg ggg aac ccc cgc tgc gat ggc cac cag cag ggt tac ccc 3544
 Asp Ser Met Gly Asn Pro Arg Cys Asp Gly His Gln Gln Gly Tyr Pro
 940 945 950

cgc aag tgg agg act gat gac gcc ccg ctc tag ggactgcagc ccagccccag 3597
 Arg Lys Trp Arg Thr Asp Asp Ala Pro Leu
 955 960

cttctctgcc cactcatttc tagtccagcc gcatttcagc agtgccttct ggggtgtccc 3657

cccacaccct gctttggccc cagaggcgag ggaccagtgg aggtgccagg gagggcccag 3717

gaccctgtgg tcccctggct ctgcctcccc accctgggggt gggggctccc ggccacctgt 3777

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ggaacctggc agaggcctta ggacccccgtt ccaagtgcac tgcccggcca agccccagcc 3957

tcagcctgcg cctgagctgc atgcgccacc atttttggca gcgtggcagc tttgcaaggg 4017

gctggggccc tcggcggtggg gccatgcctt ctgtgtgttc tgtagtgtct gggatttgcc 4077

ggtgctcaat aaatgtttat tcattgaaaa aaaaaaaaaa a 4118

<210> 5

<211> 963

<212> PRT

<213> Homo sapiens

<400> 5

Met Pro Arg Val Val Gly Pro Gly Ala Asn Leu Cys Phe Gln Val Arg
1 5 10 15

Glu Arg Gly Ser Cys Cys Ser Ser Arg Leu Arg Leu Ala Ala Asn His
20 25 30

Ile Trp Glu Trp Pro Pro Cys Ala Pro Val Ile Thr Thr Val Ala Leu
35 40 45

Lys Gln Leu Ala Ala Leu Leu Leu Val His Val Gly Gly Gly Phe Leu
50 55 60

Glu Pro Pro Pro Leu Ala Gly Phe Cys Leu Thr Pro Leu Ser Phe Pro
65 70 75 80

Cys Arg Leu Ser Ser Ala Asp Gly Pro Gly Ala Gly Met Ala Asp Ser
85 90 95

Ser Glu Gly Pro Arg Ala Gly Pro Gly Glu Val Ala Glu Leu Pro Gly
100 105 110

Asp Glu Ser Gly Thr Pro Gly Gly Glu Ala Phe Pro Leu Ser Ser Leu
115 120 125

Ala Asn Leu Phe Glu Gly Glu Asp Gly Ser Leu Ser Pro Ser Pro Ala

130 135 140
 Asp Ala Ser Arg Pro Ala Gly Pro Gly Asp Gly Arg Pro Asn Leu Arg
 145 150 155 160
 Met Lys Phe Gln Gly Ala Phe Arg Lys Gly Val Pro Asn Pro Ile Asp
 165 170 175
 Leu Leu Glu Ser Thr Leu Tyr Glu Ser Ser Val Val Pro Gly Pro Lys
 180 185 190
 Lys Ala Pro Met Asp Ser Leu Phe Asp Tyr Gly Thr Tyr Arg His His
 195 200 205
 Ser Ser Asp Asn Lys Arg Trp Arg Lys Lys Ile Ile Glu Lys Gln Pro
 210 215 220
 Gln Ser Pro Lys Ala Pro Ala Pro Gln Pro Pro Pro Ile Leu Lys Val
 225 230 235 240
 Phe Asn Arg Pro Ile Leu Phe Asp Ile Val Ser Arg Gly Ser Thr Ala
 245 250 255
 Asp Leu Asp Gly Leu Leu Pro Phe Leu Leu Thr His Lys Lys Arg Leu
 260 265 270
 Thr Asp Glu Glu Phe Arg Glu Pro Ser Thr Gly Lys Thr Cys Leu Pro
 275 280 285
 Lys Ala Leu Leu Asn Leu Ser Asn Gly Arg Asn Asp Thr Ile Pro Val
 290 295 300
 Leu Leu Asp Ile Ala Glu Arg Thr Gly Asn Met Arg Glu Phe Ile Asn
 305 310 315 320
 Ser Pro Phe Arg Asp Ile Tyr Tyr Arg Gly Gln Thr Ala Leu His Ile
 325 330 335

B1

Ala Ile Glu Arg Arg Cys Lys His Tyr Val Glu Leu Leu Val Ala Gln
 340 345 350

Gly Ala Asp Val His Ala Gln Ala Arg Gly Arg Phe Phe Gln Pro Lys
 355 360 365

Asp Glu Gly Gly Tyr Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala
 370 375 380

Ala Cys Thr Asn Gln Pro His Ile Val Asn Tyr Leu Thr Glu Asn Pro
 385 390 395 400

His Lys Lys Ala Asp Met Arg Arg Gln Asp Ser Arg Gly Asn Thr Val
 405 410 415

Leu His Ala Leu Val Ala Ile Ala Asp Asn Thr Arg Glu Asn Thr Lys
 420 425 430

Phe Val Thr Lys Met Tyr Asp Leu Leu Leu Lys Cys Ala Arg Leu
 435 440 445

Phe Pro Asp Ser Asn Leu Glu Ala Val Leu Asn Asn Asp Gly Leu Ser
 450 455 460

Pro Leu Met Met Ala Ala Lys Thr Gly Lys Ile Gly Ile Phe Gln His
 465 470 475 480

Ile Ile Arg Arg Glu Val Thr Asp Glu Asp Thr Arg His Leu Ser Arg
 485 490 495

Lys Ser Lys Asp Trp Ala Tyr Gly Pro Val Tyr Ser Ser Leu Tyr Asp
 500 505 510

Leu Ser Ser Leu Asp Thr Cys Gly Glu Glu Ala Ser Val Leu Glu Ile
 515 520 525

Leu Val Tyr Asn Ser Lys Ile Glu Asn Arg His Glu Met Leu Ala Val

B1

530 535 540
 Glu Pro Ile Asn Glu Leu Leu Arg Asp Lys Trp Arg Lys Phe Gly Ala
 545 550 555 560
 Val Ser Phe Tyr Ile Asn Val Val Ser Tyr Leu Cys Ala Met Val Ile
 565 570 575

 Phe Thr Leu Thr Ala Tyr Tyr Gln Pro Leu Glu Gly Thr Pro Pro Tyr
 580 585 590

 Pro Tyr Arg Thr Thr Val Asp Tyr Leu Arg Leu Ala Gly Glu Val Ile
 595 600 605

 Thr Leu Phe Thr Gly Val Leu Phe Phe Phe Thr Asn Ile Lys Asp Leu
 610 615 620

 Phe Met Lys Lys Cys Pro Gly Val Asn Ser Leu Phe Ile Asp Gly Ser
 625 630 635 640

 Phe Gln Leu Leu Tyr Phe Ile Tyr Ser Val Leu Val Ile Val Ser Ala
 645 650 655

 Ala Leu Tyr Leu Ala Gly Ile Glu Ala Tyr Leu Ala Met Met Val Phe
 660 665 670

 Ala Leu Val Leu Gly Trp Met Asn Ala Leu Tyr Phe Thr Arg Gly Leu
 675 680 685

 Lys Leu Thr Gly Thr Tyr Ser Ile Met Ile Gln Lys Ile Leu Phe Lys
 690 695 700

 Asp Leu Phe Arg Phe Leu Leu Val Tyr Leu Leu Phe Met Ile Gly Tyr
 705 710 715 720

 Ala Ser Ala Leu Val Ser Leu Leu Asn Pro Cys Ala Asn Met Lys Val
 725 730 735

B1

Cys Asn Glu Asp Gln Thr Asn Cys Thr Val Pro Thr Tyr Pro Ser Cys
 740 745 750

Arg Asp Ser Glu Thr Phe Ser Thr Phe Leu Leu Asp Leu Phe Lys Leu
 755 760 765

Thr Ile Gly Met Gly Asp Leu Glu Met Leu Ser Ser Thr Lys Tyr Pro
 770 775 780

Val Val Phe Ile Ile Leu Leu Val Thr Tyr Ile Ile Leu Thr Ser Val
 785 790 795 800

Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu Thr Val Gly Gln
 805 810 815

Val Ser Lys Glu Ser Lys His Ile Trp Lys Leu Gln Trp Ala Thr Thr
 820 825 830

Ile Leu Asp Ile Glu Arg Ser Phe Pro Val Phe Leu Arg Lys Ala Phe
 835 840 845

Arg Ser Gly Glu Met Val Thr Val Gly Lys Ser Ser Asp Gly Thr Pro
 850 855 860

Asp Arg Arg Trp Cys Phe Arg Val Asp Glu Val Asn Trp Ser His Trp
 865 870 875 880

Asn Gln Asn Leu Gly Ile Ile Asn Glu Asp Pro Gly Lys Asn Glu Thr
 885 890 895

Tyr Gln Tyr Tyr Gly Phe Ser His Thr Val Gly Arg Leu Arg Arg Asp
 900 905 910

Arg Trp Ser Ser Val Val Pro Arg Val Val Glu Leu Asn Lys Asn Ser
 915 920 925

Asn Pro Asp Glu Val Val Val Pro Leu Asp Ser Met Gly Asn Pro Arg
 930 935 940

Cys Asp Gly His Gln Gln Gly Tyr Pro Arg Lys Trp Arg Thr Asp Asp
 945 950 955 960

Ala Pro Leu

<210> 6

<211> 764

<212> PRT

<213> Homo sapiens

<400> 6

Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg Leu Glu Thr Leu Asp
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Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg Gly Lys Leu Asp Phe
 20 25 30

B1 Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
 35 40 45

Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
 50 55 60

Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe
 65 70 75 80

Asn Ala Val Ser Arg Gly Val Pro Glu Asp Leu Ala Gly Leu Pro Glu
 85 90 95

Tyr Leu Ser Lys Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu
 100 105 110

Gly Ser Thr Gly Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys
 115 120 125

Asp Gly Val Asn Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp

Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys Glu Glu Asn
 340 345 350

Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro His Arg His
 355 360 365

Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln Ala Lys Trp
 370 375 380

Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys Asn Leu Ile
 385 390 395 400

Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro Thr Leu Lys
 405 410 415

Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn Ser Met Leu
 420 425 430

Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr Leu Leu Val
 435 440 445

Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile Trp Ile Ser
 450 455 460

Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln Ala Leu Leu
 465 470 475 480

Thr Val Val Ser Gln Val Leu Cys Phe Leu Ala Ile Glu Trp Tyr Leu
 485 490 495

Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr
 500 505 510

Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln
 515 520 525

Lys Val Ile Leu Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val
 530 535 540

B1

130						135						140					
Ser	Gly	Asn	Pro	Gln	Pro	Leu	Val	Asn	Ala	Gln	Cys	Thr	Asp	Asp	Tyr		
145					150					155					160		
Tyr	Arg	Gly	His	Ser	Ala	Leu	His	Ile	Ala	Ile	Glu	Lys	Arg	Ser	Leu		
				165					170					175			
Gln	Cys	Val	Lys	Leu	Leu	Val	Glu	Asn	Gly	Ala	Asn	Val	His	Ala	Arg		
			180					185					190				
Ala	Cys	Gly	Arg	Phe	Phe	Gln	Lys	Gly	Gln	Gly	Thr	Cys	Phe	Tyr	Phe		
		195					200					205					
Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Lys	Gln	Trp	Asp	Val		
	210					215					220						
Val	Ser	Tyr	Leu	Leu	Glu	Asn	Pro	His	Gln	Pro	Ala	Ser	Leu	Gln	Ala		
225					230					235					240		
Thr	Asp	Ser	Gln	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val	Met	Ile	Ser		
				245					250					255			
Asp	Asn	Ser	Ala	Glu	Asn	Ile	Ala	Leu	Val	Thr	Ser	Met	Tyr	Asp	Gly		
			260					265					270				
Leu	Leu	Gln	Ala	Gly	Ala	Arg	Leu	Cys	Pro	Thr	Val	Gln	Leu	Glu	Asp		
		275					280					285					
Ile	Arg	Asn	Leu	Gln	Asp	Leu	Thr	Pro	Leu	Lys	Leu	Ala	Ala	Lys	Glu		
	290					295					300						
Gly	Lys	Ile	Glu	Ile	Phe	Arg	His	Ile	Leu	Gln	Arg	Glu	Phe	Ser	Gly		
305					310					315					320		
Leu	Ser	His	Leu	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Cys	Tyr	Gly	Pro	Val		
				325					330						335		

Phe Leu Phe Gly Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala
 545 550 555 560

Trp Arg Pro Glu Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln
 565 570 575

Pro Met Glu Gly Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly
 580 585 590

Ile Leu Glu Ala Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly
 595 600 605

Glu Leu Ala Phe Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu
 610 615 620

Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met
 625 630 635 640

Leu Ile Ala Leu Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser
 645 650 655

Trp Ser Ile Trp Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu
 660 665 670

Asn Gly Tyr Trp Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu
 675 680 685

Thr Val Gly Thr Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe
 690 695 700

Arg Val Glu Glu Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr
 705 710 715 720

Leu Cys Glu Asp Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn
 725 730 735

Pro Val Leu Ala Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu

B1

37

740

745

750

B1 Glu Asn Tyr Val Pro Val Gln Leu Leu Gln Ser Asn

755

760

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 <211> 18
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 atttaggtga cactatag 18

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 8
 taatagcact cactataggg 20

<210> 9
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
 ggaaacagct atgaccatg 19

B1

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<211> 17

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B1

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B1

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20

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B1

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B1

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1

5

10

15

Asp Ser Glu Glu Ala Ser Cys

B1

20

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<212> PRT

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<223> Description of Artificial Sequence: Synthetic
sequence

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Cys Gly Ser Leu Lys Pro Glu Asp Ala Glu Val Phe Lys Asp Ser Met

1

5

10

15

Val Pro Gly Glu Lys

20

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<210> 30

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B1

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B1

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acaagaaggc ggacatgcgg

20

B1

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<223> Description of Artificial Sequence: Primer

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atctcgtggc ggttctcaat

20

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1

ERROR LISTING
PATENT APPLICATION

DATE:
TIME:

12:07:35

INPUT SEQ: A:\Pg3606SEQLIST.txt

L:1727 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:20 SEQ:40

B1